

5' TGG CGC TTG CCG AGT GAT TCT CCT CGA ATA CCT CCT GCC GGC GCG GAG ACA CCG
 10 19 28 37 46 55
 GGG CGG GGG TCC TGC CGC AAC TAC CTC CCT TCC TCC TCT CCC CCG CCC CCG GAG
 64 73 82 91 100 109
 CCT TCA TCC TTC CCT TCC CCC CCC ACC TCG AGG GGC GGG CCT GGT TCC CGG GAC
 118 127 136 145 154 163
 ACC ATG TCG GAC TCT GAG GAG AGC CAG GAC CGG CAA CTG AAA ATC GTC GTG
 172 181 190 199 208 217
 M S D S E E E S Q D R Q L K I V V
 CTG GGG GAC GNN GCC TCC GGG AAG ACC TCC TTA ACT ACG TGT TTT GCT CAA GAA
 226 235 244 253 262 271
 L G D X A S G K T S L T T C F A Q E
 ACT TTT GGG AAA CAG TAC AAA CAA ACT ATA GGA CTG GAT TTC TTT TTG AGA AGG
 280 289 298 307 316 325
 T F G K Q Y K Q T I G L D F F L R R
 ATA ACA TTG CCA GGA AAC TTG AAT GTT ACC CTT CAA ATT TGG GAT ATA GGA GGG
 334 343 352 361 370 379
 I T L P G N L N V T L Q I W D I G G
 CAG ACA ATA GGA GGC AAA ATG TTG GAT AAA TAT ATC TAT GGA GCA CAG GGA GTC
 388 397 406 415 424 433
 Q T I G G K M L D K Y I Y G A Q G V
 CTC TTG GTA TAT GAT ATT ACA AAT TAT CAA AGC TTT GAG AAT TTA GAA GAT TGG
 442 451 460 469 478 487
 L L V Y D I T N Y Q S F E N L E D W
 TAT ACT GTG GTG AAG AAA GTG AGC NAG GAG TCA GAA ACT CAG CCA CTG GTT GCC
 496 505 514 523 532 541
 Y T V V K K V S X E S E T Q P L V A
 TTG GTA GGC AAT AAA ATT GAT TTG GAG CAT ATG CGA ACA ATA AAA CCT GAA AAA
 550 559 568 577 586 595
 L V G N K I D L E H M R T I K P E K
 CAC TTA CGG TTT TGC CAG GAA AAT GGT TTT AGT AGC CAC TTT GTC TCA GCC AAG
 604 613 622 631 640 649
 H L R F C Q E N G F S S H F V S A K
 ACA GGA GAC TCT GTC TTC CTG TGC TTT CAG AAA GTT GCT GCT GAA ATC CTT GGG
 658 667 676 685 694 703
 T G D S V F L C F Q K V A A E I L G

FIGURE 1A

0988974.11901

[illegible]

ATC	AAA	712	TTA	AAC	AAN	721	NAG	CAG	AAW	730	TRG	MAC	AGT	739	CAC	AGW	GGG	748	GTG	GTG	AAG	757	GSA
I	K	L	N	X	X	Q	X	X	X	X	X	S	H	X	G	V	V	K	X				
GRT	ATT	766	GTA	AAC	TAC	775	AAC	CAG	GAA	784	CCT	ATG	TCA	793	AGG	ACT	KTT	802	AAC	CCT	CCT	811	AGA
X	I	V	N	Y	N	Q	E	P	M	S	R	T	X	N	P	P	R						
AGC	TCT	820	ATG	TGT	GCA	829	GTT	CAG	TGA	838	GCG	CAT	TTT	847	NCT	TTT	GTN	856	TTG	ATA	GTT	865	CTG
S	S	M	C	A	V	Q																	
GCT	GCC	874	CTT	CAA	CTC	883	TGG	GTG	GGN	892	CCC	NAG	GGC	901	TTC	TAG	GAC	910	TTG	TTT	T	3'	

[illegible]

FIGURE 1B

5' GCA TTG AGC CAA CAC ACA GAT TTG TCG CCT CTG TCC CCG AAG ACA CCT GCA CCC
10 19 28 37 46 55
TCC ATG CGG ANC AAG ATG GGG AAT GGA ACT GAG GAA GAT TAT AAC TTT GTC TTC
64 73 82 91 100 109
M R X K M G N G T E E D Y N F V F
AAG GTG GTG CTG ATC GGC GAA TCA GGT GTG GGG AAG ACC AAT CTA CTC TCC CGA
118 127 136 145 154 163
K V V L I G E S G V G K T N L L S R
TTC ACG CGC AAT GAG TTC AGC CAC GAC AGC CGC ACC ACC ATC GGG GTT GAG TTC
172 181 190 199 208 217
F T R N E F S H D S R T T I G V E F
TCC ACC CGC ACT GTG ATG TTG GGC ACC GCT GCT GTC AAG GCT CAG ATC TGG GAC
226 235 244 253 262 271
S T R T V M L G T A A V K A Q I W D
ACA GCT GGC CTG GAG CGG TAC CGA GCC ATC ACC TCG GCG TAC TAT CGT GGT GCA
280 289 298 307 316 325
T A G L E R Y R A I T S A Y Y R G A
GTG GGG GCC CTC CTG GTG TTT GAC CTA ACC AAG CAC CAG ACC TAT GCT GTG GTG
334 343 352 361 370 379
V G A L L V F D L T K H Q T Y A V V
GAG CGA TGG CTG AAG GAG CTC TAT GAC CAT GCT GAA GCC ACG ATC GTC GTC
388 397 406 415 424 433
E R W L K E L Y D H A E A T I V V M
CTC GTG GGT AAC AAA AGT GAC CTC AGC CAG GGC CGG GAA GTG CCC ACT GAG GAG
442 451 460 469 478 487
L V G N K S D L S Q G R E V P T E E
GCC CGA ATG TTC GCT GAA AAC AAT GGA CTG CTC TTC CTG GAG ACC TCA GCC CTG
496 505 514 523 532 541
A R M F A E N N G L L F L E T S A L
GAC TCT ACC AAT GTT GAG CTA GCC TTT GAG ACT GTC CTG AAA GAA ATC TTT GCG
550 559 568 577 586 595
D S T N V E L A F E T V L K E I F A
AAG GTG TCC AAG CAG AGA CAG AAC AGC ATC CGG ACC AAT GCC ATC ACT CTG GGC
604 613 622 631 640 649
K V S K Q R Q N S I R T N A I T L G
AGT GCC CAG GNT GGA CAG GAG CCT GGC CCT GGG GAG AAG AGG GCC TGT TGC ATC
658 667 676 685 694 703
S A Q X G Q E P G P G E K R A C C I

FIGURE 2A

000000 44588660

Docket No.: PF-0183-2 DIV
Inventors: Hillman et al.
Title: RAB PROTEINS
Serial No.: To Be Assigned

712 721 730 739 748 757
AGC CTC TGA CCT TGG CCA GCA CCA CCT GCC CCC ACT GGC TTT TTG GTG CCC CTT
S L
766 775 784 793 802 811
GTC CCC ACT TCA GCC CCA GGA CCT TTC CTT GCC CTT TGG TTC CAG ATA TCA GAC
820 829 838 847
TGT TCC CTG TTC ACA GCA CCC TCA GGG TCT TAA GGT 3'

FIGURE 2B

0988974-111901

Docket No.: PF-0183-2 DIV

Inventors: Hillman et al.

Title: RAB PROTEINS

Serial No.: To Be Assigned

5' CTG TGA TGA AAC ACT TTT CCC GTG TCG TTT GAG TGC ATC TTC TCA ACA ACC CTA
11 20 29 38 47 56
GGA GGG TTC TTG AAG CTT TTG AGA TTA ACA ATG GCA GGA AAA TCA TCA CTT TTT
65 74 83 92 101 110
M A G K S S L F
AAA GTA ATT CTC CTT GGA GAT GGT GGA GTT GGG AAG AGT TCA CTT ATG AAC AGA
119 128 137 146 155 164
K V I L L G D G G V G K S S L M N R
TAT GTA ACT AAT AAG TTT GAT ACC CAG CTC TTC CAT ACA ATA GGT GTG GAA TTT
173 182 191 200 209 218
Y V T N K F D T Q L F H T I G V E F
TTA AAT AAA GAT TTG GAA GTG GAT GGA CAT TTT GTT ACC ATG CAG ATT TGG GAC
227 236 245 254 263 272
L N K D L E V D G H F V T M Q I W D
ACG GCA GGT CAG GAG CGA TTC CGA AGC CTG AGG ACA CCA TTT TAC AGA GGT TCT
281 290 299 308 317 326
T A G Q E R F R S L R T P F Y R G S
GAC TGC TGC CTG CTT ACT TTT AGT GTC GAT GAT TCA CAA AGC TTC CAG AAC TTA
335 344 353 362 371 380
D C C L L T F S V D D S Q S F Q N L
AGT AAC TGG AAG AAA GAA TTC ATA TAT TAT GCA GAT GTG AAA GAG CCT GAG AGC
389 398 407 416 425 434
S N W K K E F I Y Y A D V K E P E S
TTT CCT TTT GTG ATT CTG GGT AAC AAG ATT GAC ATA AGC GAA CGG CAG GTG TCT
443 452 461 470 479 488
F P F V I L G N K I D I S E R Q V S
ACA GAA GAA GCC CAA GCT TGG TGC AGG GAC AAC GGC GAC TAT CCT TAT TTT GAA
497 506 515 524 533 542
T E E A Q A W C R D N G D Y P Y F E
ACA AGT GCA AAA GAT GCC ACA AAT GTG GCA GCA GCC TTT GAG GAA GCG GTT CGA
551 560 569 578 587 596
T S A K D A T N V A A A F E E A V R
AGA GTT CTT GCT ACC GAG GAT AGG TCA GAT CAT TTG ATT CAG ACA GAC ACA GTC
605 614 623 632 641 650
R V L A T E D R S D H L I Q T D T V

FIGURE 3A

Docket No.: PF-0183-2 DIV

Inventors: Hillman et al.

Title: RAB PROTEINS

Serial No.: To Be Assigned

659 668 677 686 695 704
AAT CTT CAC CGA AAG CCC AAG CCT AGC TCA TCT TGC TGT TGA TTG TTA GAT TGT
N L H R K P K P S S S C C
713 722 731 740 749 758
TGA TGC ATT CTA ACC AAC TCA CAC ATA TAC ACA AAA TCA ACA TGG GGA TGG AGA
767 776 785 794 803 812
AGA GAA TTA GCG TTT GCA GCA GTG TAT CAT CTA CTA ATA AAA TTA AAC TAA TGT
821 830 839 848 857 866
TGC TGC TTC ATT AGT TGG TGG GAG AAG GGA CAC ATC CAC TCT TGG AGG AAT ATA
875 884 893 902 911 920
TTT ACT CAA TAA TGG CAC CTT ACA TTT ATA AAT TGT AAC AGT TGT CTA ATA ACG
929 938 947 956 965 974
TTT CTT TAA TTT AAA TAT GTA AGT TGC AGA GCT AAT AAA TGA AAT GAC CAA GAC
983 992 1001 1010 1019 1028
TTT AAT TAT AAT AAA AAT AAG AAA CTT GAC TAT TCT AGA AGT TAT ACT TGG ATT
1037 1046 1055 1064 1073 1082
TTT TCC TGG GAA AAT GGA GAA CTA CTT TTT ATA TGT GTA TGT TTT TAT GCA ATT
1091 1100 1109 1118 1127 1136
AGC ATT GTA TTC TTG GTT CAG GGA AAT ACT TTC CTA AAG CAA TAA TGT TAG ATA
1145 1154 1163 1172
TTA AAG ATT AAA ATC TAA TGT AAA AAA AAA AAA AAA AAA 3'

FIGURE 3B

1	M	S	D	S	E	E	S	Q	D	R	Q	-	-	-	-	L	K	I	V	V	L	G	D	X	A	S	G	K	T	SEQ ID NO-1	
1	M	S	D	S	E	E	S	Q	D	R	Q	-	-	-	-	L	K	I	V	V	L	G	D	G	T	S	G	K	T	GI 1154901	
1	M	R	X	K	M	G	N	G	T	E	E	D	Y	N	F	V	F	K	V	V	L	I	G	E	S	G	V	G	K	T	SEQ ID NO-3
1	M	G	N	-	-	-	-	G	K	E	E	D	Y	N	F	V	F	K	V	V	L	I	G	E	S	G	V	G	K	T	GI 436001
1	M	A	G	K	S	S	-	-	-	-	-	-	-	-	-	L	F	K	V	I	L	L	G	D	G	G	V	G	K	S	SEQ ID NO-5
1	M	A	G	K	S	S	-	-	-	-	-	-	-	-	-	L	F	K	V	I	L	L	G	D	G	G	V	G	K	S	GI 486830
27	S	L	T	T	C	F	A	Q	E	T	F	G	K	Q	Y	K	Q	T	I	G	L	D	F	F	L	R	R	I	T	L	SEQ ID NO-1
27	S	L	A	T	C	F	A	Q	E	T	F	G	K	Q	Y	K	Q	T	I	G	L	D	F	F	L	R	R	I	T	L	GI 1154901
31	N	L	L	S	R	F	T	R	N	E	F	S	H	D	S	R	T	T	I	G	V	E	F	S	T	R	T	V	M	L	SEQ ID NO-3
27	N	L	L	S	R	F	T	R	N	E	F	S	H	D	S	R	T	T	I	G	V	E	F	S	T	R	T	V	M	L	GI 436001
22	S	L	M	N	R	Y	V	T	N	K	F	D	T	Q	L	F	H	T	I	G	V	E	F	L	N	K	D	L	E	V	SEQ ID NO-5
22	S	L	M	N	R	Y	V	T	N	K	F	D	T	Q	L	F	H	T	I	G	V	E	F	L	N	K	D	L	E	V	GI 486830
57	P	G	N	L	N	V	T	L	Q	I	W	D	I	G	G	Q	T	I	G	G	K	M	L	D	K	Y	I	Y	G	A	SEQ ID NO-1
57	P	G	N	L	N	V	T	L	Q	I	W	D	I	G	G	Q	T	I	G	G	K	M	L	D	K	Y	I	Y	G	A	GI 1154901
61	G	T	A	A	-	V	K	A	Q	I	W	D	T	A	G	L	E	R	Y	R	A	I	T	S	A	Y	Y	R	G	A	SEQ ID NO-3
57	G	T	A	A	-	V	K	A	Q	I	W	D	T	A	G	L	E	R	Y	R	A	I	T	S	A	Y	Y	R	G	A	GI 436001
52	D	G	H	F	-	V	T	M	Q	I	W	D	T	A	G	Q	E	R	F	R	S	L	R	T	P	F	Y	R	G	S	SEQ ID NO-5
52	D	G	H	F	-	V	T	M	Q	I	W	D	T	A	G	Q	E	R	F	R	S	L	R	T	P	F	Y	R	G	S	GI 486830
87	Q	G	V	L	L	V	Y	D	I	T	N	Y	Q	S	F	E	N	L	E	D	W	Y	T	V	V	K	K	V	S	X	SEQ ID NO-1
87	Q	G	I	L	L	V	Y	D	I	T	N	Y	Q	S	F	E	N	L	E	D	W	Y	S	V	V	K	T	V	S	E	GI 1154901
90	V	G	A	L	L	V	F	D	L	T	K	H	Q	T	Y	A	V	V	E	R	W	L	K	E	L	-	-	Y	D	H	SEQ ID NO-3
86	V	G	A	L	L	V	F	D	L	T	K	H	Q	T	Y	A	V	V	E	R	W	L	K	E	L	-	-	Y	D	H	GI 436001
81	D	C	C	L	L	T	F	S	V	D	D	S	Q	S	F	Q	N	L	S	N	W	K	K	E	F	I	Y	Y	A	D	SEQ ID NO-5
81	D	C	C	L	L	T	F	S	V	D	D	S	Q	S	F	Q	N	L	S	N	W	K	K	E	F	I	Y	Y	A	D	GI 486830
117	E	S	E	T	Q	P	L	V	-	A	L	V	G	N	K	I	D	L	E	H	M	R	T	I	K	P	E	K	H	L	SEQ ID NO-1
117	E	S	E	T	Q	P	L	V	-	A	L	V	G	N	K	I	D	L	E	H	M	R	T	V	K	P	D	K	H	L	GI 1154901
118	A	E	A	-	-	T	I	V	V	M	L	V	G	N	K	S	D	L	S	Q	G	R	E	V	P	T	E	E	A	R	SEQ ID NO-3
114	A	E	A	-	-	T	I	V	V	M	L	V	G	N	K	S	D	L	S	Q	A	R	E	V	P	T	E	E	A	R	GI 436001
111	V	K	E	P	E	S	F	P	F	V	I	L	G	N	K	I	D	I	S	E	-	R	Q	V	S	T	E	E	A	Q	SEQ ID NO-5
111	V	K	E	P	E	S	F	P	F	V	I	L	G	N	K	I	D	I	S	E	-	R	Q	V	S	T	E	E	A	Q	GI 486830
146	R	F	C	Q	E	N	G	F	S	S	H	F	-	V	S	A	K	T	G	D	S	V	F	L	C	F	Q	K	V	A	SEQ ID NO-1
146	R	F	C	Q	E	N	G	F	S	S	H	F	-	V	S	A	K	T	G	D	S	V	F	L	C	F	Q	K	V	A	GI 1154901
146	M	F	A	E	N	N	G	-	L	L	F	L	E	T	S	A	L	D	S	T	N	V	E	L	A	F	E	T	V	L	SEQ ID NO-3
142	M	F	A	E	N	N	G	-	L	L	F	L	E	T	S	A	L	D	S	T	N	V	E	L	A	F	E	T	V	L	GI 436001
140	A	W	C	R	D	N	G	D	Y	P	Y	F	E	T	S	A	K	D	A	T	N	V	A	A	A	F	E	E	A	V	SEQ ID NO-5
140	A	W	C	R	D	N	G	D	Y	P	Y	F	E	T	S	A	K	D	A	T	N	V	A	A	A	F	E	E	A	V	GI 486830
175	A	E	I	L	G	I	K	L	N	X	X	Q	X	X	X	S	H	X	G	V	V	K	X	X	I	V	N	Y	N	Q	SEQ ID NO-1
175	A	E	I	L	G	I	K	L	N	K	A	E	I	E	Q	S	Q	R	-	V	V	K	A	D	I	V	N	Y	N	Q	GI 1154901
175	K	E	I	F	-	-	-	-	-	-	A	K	V	S	K	Q	R	Q	N	S	I	R	T	N	A	I	T	L	G	S	SEQ ID NO-3
171	K	E	I	F	-	-	-	-	-	-	A	K	V	S	K	Q	I	Q	N	S	P	R	S	N	A	I	A	L	G	S	GI 436001
170	R	R	V	L	-	-	-	-	-	-	A	T	-	E	D	R	S	D	H	L	I	Q	T	D	T	V	N	L	-	-	SEQ ID NO-5
170	R	R	V	L	-	-	-	-	-	-	A	T	-	E	D	R	S	D	H	L	I	Q	T	D	T	V	S	L	-	-	GI 486830
205	E	P	M	S	R	T	X	N	P	P	R	S	S	M	C	A	V	Q													SEQ ID NO-1
204	E	P	M	S	R	T	V	N	P	P	R	S	S	M	C	A	V	Q													GI 1154901
199	A	Q	X	G	Q	E	P	G	P	G	E	K	R	A	C	C	I	S	L												SEQ ID NO-3
195	A	Q	A	G	Q	E	P	G	P	G	Q	K	R	A	C	C	I	N	L												GI 436001
191	-	-	-	-	-	H	R	K	P	K	P	S	S	S	C	C															SEQ ID NO-5
191	-	-	-	-	-	H	R	K	P	K	P	S	S	S	C	C															GI 486830

0988974-11901

FIGURE 4

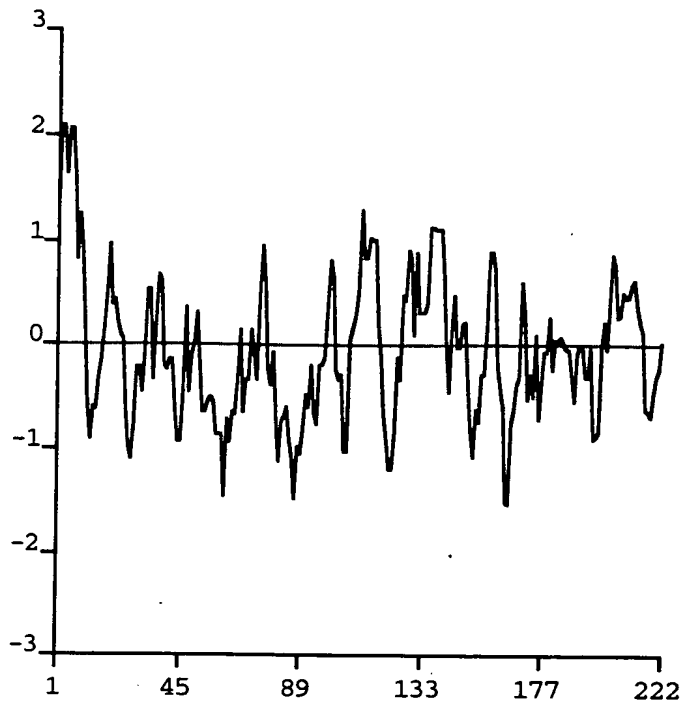


FIGURE 5

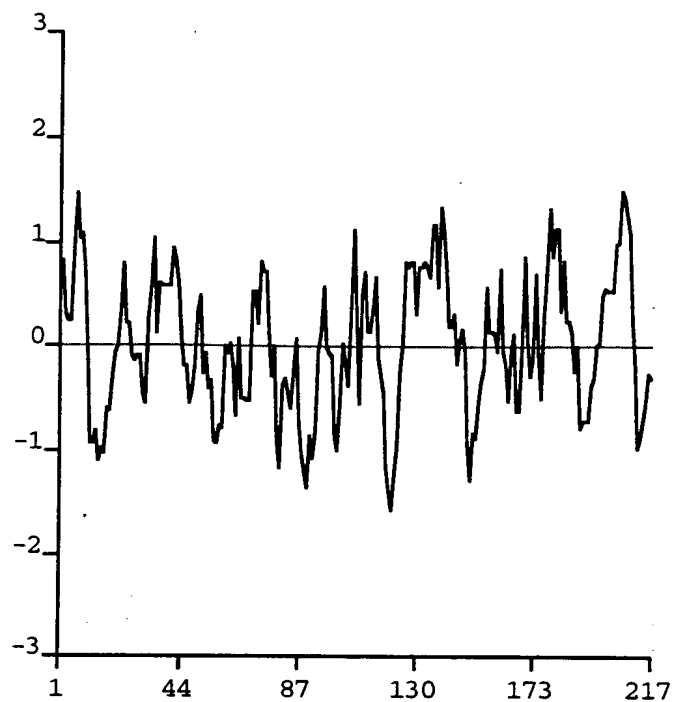


FIGURE 6

0988974-11901

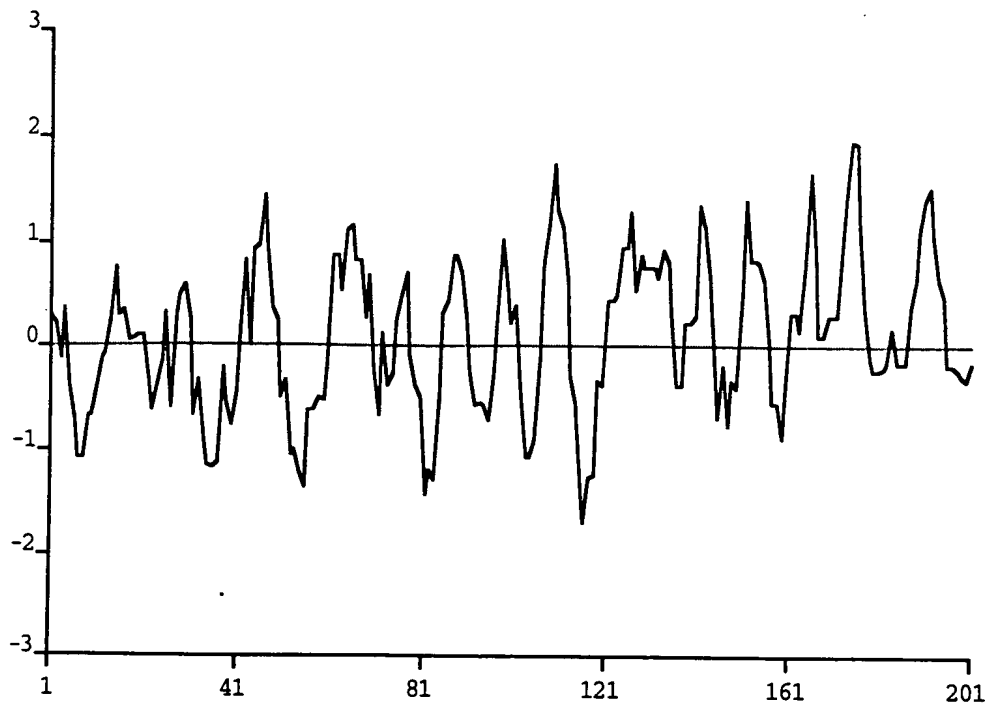


FIGURE 7

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FIGURE 8